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RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/996,569

DATE: 12/06/2001

TIME: 15:04:44

Input Set : A:\PF201D2-SeqList-text.txt

Output Set: N:\CRF3\12062001\I996569.raw

ENTERED

3 <110> APPLICANT: Soppet et al.
 5 <120> TITLE OF INVENTION: G-Protein Parathyroid Hormone Receptor HLTDG74
 7 <130> FILE REFERENCE: PF201D1
 C--> 9 <140> CURRENT APPLICATION NUMBER: US/09/996,569
 C--> 10 <141> CURRENT FILING DATE: 2001-11-30
 12 <150> PRIOR APPLICATION NUMBER: 08/468,011
 13 <151> PRIOR FILING DATE: 1995-06-06
 15 <160> NUMBER OF SEQ ID NOS: 28
 17 <170> SOFTWARE: PatentIn Ver. 2.1
 19 <210> SEQ ID NO: 1
 20 <211> LENGTH: 2003
 21 <212> TYPE: DNA
 22 <213> ORGANISM: Homo sapiens
 24 <220> FEATURE:
 25 <221> NAME/KEY: CDS
 26 <222> LOCATION: (90)..(1715)
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 32 Met Ala Trp Leu Gly Ala Ser Leu
 33 1 5
 35 cac gtc tgg ggt tgg cta atg ctc ggc agc tgc ctc ctg gcc aga gcc 161
 36 His Val Trp Gly Trp Leu Met Leu Gly Ser Cys Leu Leu Ala Arg Ala
 37 10 15 20
 39 cag ctg gat tct gat ggc acc atc act ata gag gag cag att gtc ctt 209
 40 Gln Leu Asp Ser Asp Gly Thr Ile Thr Ile Glu Glu Gln Ile Val Leu
 41 25 30 35 40
 43 gtg ctg aaa gcg aaa gta caa tgt gaa ctc aac atc aca gct caa ctc 257
 44 Val Leu Lys Ala Lys Val Gln Cys Glu Leu Asn Ile Thr Ala Gln Leu
 45 45 50 55
 47 cag gag gga gaa ggt aat tgt ttc cct gaa tgg gat gga ctc att tgt 305
 48 Gln Glu Gly Glu Gly Asn Cys Phe Pro Glu Trp Asp Gly Leu Ile Cys
 49 60 65 70
 51 tgg ccc aga gga aca gtg ggg aaa ata tcg gct gtt cca tgc cct cct 353
 52 Trp Pro Arg Gly Thr Val Gly Lys Ile Ser Ala Val Pro Cys Pro Pro
 53 75 80 85
 55 tat att tat gac ttc aac cat aaa gga gtt gct ttc cga cac tgt aac 401
 56 Tyr Ile Tyr Asp Phe Asn His Lys Gly Val Ala Phe Arg His Cys Asn
 57 90 95 100
 59 ccc aat gga aca tgg gat ttt atg cac agc tta aat aaa aca tgg gcc 449
 60 Pro Asn Gly Thr Trp Asp Phe Met His Ser Leu Asn Lys Thr Trp Ala
 61 105 110 115 120
 63 aat tat tca gac tgc ctt cgc ttt ctg cag cca gat atc agc ata gga 497
 64 Asn Tyr Ser Asp Cys Leu Arg Phe Leu Gln Pro Asp Ile Ser Ile Gly
 65 125 130 135
 67 aag caa gaa ttc tgt gaa cgc ctc tat gta atg tat acc gtt gcc tac 545
 68 Lys Gln Glu Phe Cys Glu Arg Leu Tyr Val Met Tyr Thr Val Gly Tyr

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69	140	145	150	
71	tcc atc tct ttt ggt tcc ttg gct gtg gct att ctc atc att ggt tac	593		
72	Ser Ile Ser Phe Gly Ser Leu Ala Val Ala Ile Leu Ile Ile Gly Tyr			
73	155	160	165	
75	ttc aga cga ttg cat tgc act agg aac tat atc cac atg cac tta ttt	641		
76	Phe Arg Arg Leu His Cys Thr Arg Asn Tyr Ile His Met His Leu Phe			
77	170	175	180	
79	gtg tct ttc atg ctg aga gct aca agc atc ttt gtc aaa gac aga gta	689		
80	Val Ser Phe Met Leu Arg Ala Thr Ser Ile Phe Val Lys Asp Arg Val			
81	185	190	195	200
83	gtc cat gct cac ata gga gta aag gag ctg gag tcc cta ata atg cag	737		
84	Val His Ala His Ile Gly Val Lys Glu Leu Glu Ser Leu Ile Met Gln			
85	205	210	215	
87	gat gac cca caa aat tcc att gag gca act tct gtg gac aaa tca caa	785		
88	Asp Asp Pro Gln Asn Ser Ile Glu Ala Thr Ser Val Asp Lys Ser Gln			
89	220	225	230	
91	tat atc ggg tgc aag att gct gtt gtg atg ttt att tac ttc ctg gct	833		
92	Tyr Ile Gly Cys Lys Ile Ala Val Val Met Phe Ile Tyr Phe Leu Ala			
93	235	240	245	
95	aca aat tat tat tgg atc ctg gtg gaa ggt ctc tac ctg cat aat ctc	881		
96	Thr Asn Tyr Tyr Trp Ile Leu Val Glu Gly Leu Tyr Leu His Asn Leu			
97	250	255	260	
99	atc ttt gtg gct ttc ttt tcg gac acc aaa tac ctg tgg ggc ttc atc	929		
100	Ile Phe Val Ala Phe Phe Ser Asp Thr Lys Tyr Leu Trp Gly Phe Ile			
101	265	270	275	280
103	ttg ata ggc tgg ggg ttt cca gca gca ttt gtt gca gca tgg gct gtg	977		
104	Leu Ile Gly Trp Gly Phe Pro Ala Ala Phe Val Ala Ala Trp Ala Val			
105	285	290	295	
107	gca cga gca act ctg gct gat gcg agg tgc tgg gaa ctt agt gct gga	1025		
108	Ala Arg Ala Thr Leu Ala Asp Ala Arg Cys Trp Glu Leu Ser Ala Gly			
109	300	305	310	
111	gac atc aag tgg att tat caa gca ccg atc tta gca gct att ggg ctg	1073		
112	Asp Ile Lys Trp Ile Tyr Gln Ala Pro Ile Leu Ala Ala Ile Gly Leu			
113	315	320	325	
115	aat ttt att ctg ttt ctg aat acg gtt aga gtt cta gct acc aaa atc	1121		
116	Asn Phe Ile Leu Phe Leu Asn Thr Val Arg Val Leu Ala Thr Lys Ile			
117	330	335	340	
119	tgg gag acc aat gca gtt ggg cat gac aca agg aag caa tac agg aaa	1169		
120	Trp Glu Thr Asn Ala Val Gly His Asp Thr Arg Lys Gln Tyr Arg Lys			
121	345	350	355	360
123	ctg gcc aaa tcg aca ctg gtc ctg gtc cta gtc ttt gga gtg cat tac	1217		
124	Leu Ala Lys Ser Thr Leu Val Leu Val Leu Val Phe Gly Val His Tyr			
125	365	370	375	
127	atc gtg ttc gtg tgc ctg cct cac tcc ttc act ggg ctc ggg tgg gag	1265		
128	Ile Val Phe Val Cys Leu Pro His Ser Phe Thr Gly Leu Gly Trp Glu			
129	380	385	390	
131	atc cgc atg cac tgt gag ctc ttc ttc aac tcc ttt cag ggt ttc ttt	1313		
132	Ile Arg Met His Cys Glu Leu Phe Phe Asn Ser Phe Gln Gly Phe Phe			
133	395	400	405	

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135 gtg tct atc atc tac tgc tac tgc aat gga gag gtt cag gca gag gtg 1361
136 Val Ser Ile Ile Tyr Cys Tyr Cys Asn Gly Glu Val Gln Ala Glu Val
137      410      415      420
139 aag aag atg tgg agt cgg tgg aat ctc tcc gtg gac tgg aaa agg aca 1409
140 Lys Lys Met Trp Ser Arg Trp Asn Leu Ser Val Asp Trp Lys Arg Thr
141 425      430      435      440
143 ccg cca tgt ggc agc cgc aga tgc ggc tca gtg ctc acc acc gtg acg 1457
144 Pro Pro Cys Gly Ser Arg Arg Cys Gly Ser Val Leu Thr Thr Val Thr
145      445      450      455
147 cac agc acc agc agc cag tca cag gtg gcg gca gca cac gca tgg tgc 1505
148 His Ser Thr Ser Ser Gln Ser Gln Val Ala Ala Ala His Ala Trp Cys
149      460      465      470
151 tta tct ctg gca aag ctg cca aga tcg cca gca gac agc ctg aca gcc 1553
152 Leu Ser Leu Ala Lys Leu Pro Arg Ser Pro Ala Asp Ser Leu Thr Ala
153      475      480      485
155 aca tca ctt tac ctg gct atg tct gga gta act cag agc agg act gcc 1601
156 Thr Ser Leu Tyr Leu Ala Met Ser Gly Val Thr Gln Ser Arg Thr Ala
157      490      495      500
159 tca cac act ctc tcc acg agg agc aac aag gaa gat agt ggg agg cag 1649
160 Ser His Thr Leu Ser Thr Arg Ser Asn Lys Glu Asp Ser Gly Arg Gln
161 505      510      515      520
163 aga gat gat att cta atg gag aag cct tcc agg cct atg gaa tct aac 1697
164 Arg Asp Asp Ile Leu Met Glu Lys Pro Ser Arg Pro Met Glu Ser Asn
165      525      530      535
167 cca gac act gaa gga tgacaaggag aaactgagga tgttctctga atggacatgt 1752
168 Pro Asp Thr Glu Gly
169      540
171 gtggctgact ttcattgggct ggtccaatgg ctggttgtgt gagagggcctt ggctgatact 1812
173 cctatgcttg agcacaagg ctgaaaattc agttaagggtg ttacttaata atagttttta 1872
175 ggctccatga attggctcct gtaaatacta acgacatgaa aatgcaagtg tcaatggagt 1932
177 agtttattac cttctattgg catcaagttt tctctataat taatgtatgg tatttgctct 1992
179 gtgattgttc a 2003
184 <210> SEQ ID NO: 2
185 <211> LENGTH: 541
186 <212> TYPE: PRT
187 <213> ORGANISM: Homo sapiens
189 <400> SEQUENCE: 2
190 Met Ala Trp Leu Gly Ala Ser Leu His Val Trp Gly Trp Leu Met Leu
191 1      5      10      15
193 Gly Ser Cys Leu Leu Ala Arg Ala Gln Leu Asp Ser Asp Gly Thr Ile
194      20      25      30
196 Thr Ile Glu Glu Gln Ile Val Leu Val Leu Lys Ala Lys Val Gln Cys
197      35      40      45
199 Glu Leu Asn Ile Thr Ala Gln Leu Gln Glu Gly Glu Gly Asn Cys Phe
200      50      55      60
202 Pro Glu Trp Asp Gly Leu Ile Cys Trp Pro Arg Gly Thr Val Gly Lys
203 65      70      75      80
205 Ile Ser Ala Val Pro Cys Pro Pro Tyr Ile Tyr Asp Phe Asn His Lys
206      85      90      95

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208 Gly Val Ala Phe Arg His Cys Asn Pro Asn Gly Thr Trp Asp Phe Met
209          100          105          110
211 His Ser Leu Asn Lys Thr Trp Ala Asn Tyr Ser Asp Cys Leu Arg Phe
212          115          120          125
214 Leu Gln Pro Asp Ile Ser Ile Gly Lys Gln Glu Phe Cys Glu Arg Leu
215          130          135          140
217 Tyr Val Met Tyr Thr Val Gly Tyr Ser Ile Ser Phe Gly Ser Leu Ala
218 145          150          155          160
220 Val Ala Ile Leu Ile Ile Gly Tyr Phe Arg Arg Leu His Cys Thr Arg
221          165          170          175
223 Asn Tyr Ile His Met His Leu Phe Val Ser Phe Met Leu Arg Ala Thr
224          180          185          190
226 Ser Ile Phe Val Lys Asp Arg Val Val His Ala His Ile Gly Val Lys
227          195          200          205
229 Glu Leu Glu Ser Leu Ile Met Gln Asp Asp Pro Gln Asn Ser Ile Glu
230          210          215          220
232 Ala Thr Ser Val Asp Lys Ser Gln Tyr Ile Gly Cys Lys Ile Ala Val
233 225          230          235          240
235 Val Met Phe Ile Tyr Phe Leu Ala Thr Asn Tyr Tyr Trp Ile Leu Val
236          245          250          255
238 Glu Gly Leu Tyr Leu His Asn Leu Ile Phe Val Ala Phe Phe Ser Asp
239          260          265          270
241 Thr Lys Tyr Leu Trp Gly Phe Ile Leu Ile Gly Trp Gly Phe Pro Ala
242          275          280          285
244 Ala Phe Val Ala Ala Trp Ala Val Ala Arg Ala Thr Leu Ala Asp Ala
245          290          295          300
247 Arg Cys Trp Glu Leu Ser Ala Gly Asp Ile Lys Trp Ile Tyr Gln Ala
248 305          310          315          320
250 Pro Ile Leu Ala Ala Ile Gly Leu Asn Phe Ile Leu Phe Leu Asn Thr
251          325          330          335
253 Val Arg Val Leu Ala Thr Lys Ile Trp Glu Thr Asn Ala Val Gly His
254          340          345          350
256 Asp Thr Arg Lys Gln Tyr Arg Lys Leu Ala Lys Ser Thr Leu Val Leu
257          355          360          365
259 Val Leu Val Phe Gly Val His Tyr Ile Val Phe Val Cys Leu Pro His
260          370          375          380
262 Ser Phe Thr Gly Leu Gly Trp Glu Ile Arg Met His Cys Glu Leu Phe
263 385          390          395          400
265 Phe Asn Ser Phe Gln Gly Phe Phe Val Ser Ile Ile Tyr Cys Tyr Cys
266          405          410          415
268 Asn Gly Glu Val Gln Ala Glu Val Lys Lys Met Trp Ser Arg Trp Asn
269          420          425          430
271 Leu Ser Val Asp Trp Lys Arg Thr Pro Pro Cys Gly Ser Arg Arg Cys
272          435          440          445
274 Gly Ser Val Leu Thr Thr Val Thr His Ser Thr Ser Ser Gln Ser Gln
275          450          455          460
277 Val Ala Ala Ala His Ala Trp Cys Leu Ser Leu Ala Lys Leu Pro Arg
278 465          470          475          480
280 Ser Pro Ala Asp Ser Leu Thr Ala Thr Ser Leu Tyr Leu Ala Met Ser

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281              485              490              495
283 Gly Val Thr Gln Ser Arg Thr Ala Ser His Thr Leu Ser Thr Arg Ser
284              500              505              510
286 Asn Lys Glu Asp Ser Gly Arg Gln Arg Asp Asp Ile Leu Met Glu Lys
287              515              520              525
289 Pro Ser Arg Pro Met Glu Ser Asn Pro Asp Thr Glu Gly
290              530              535              540
294 <210> SEQ ID NO: 3
295 <211> LENGTH: 23
296 <212> TYPE: DNA
297 <213> ORGANISM: Artificial Sequence
299 <220> FEATURE:
300 <221> NAME/KEY: Primer_Bind
301 <223> OTHER INFORMATION: This 5' primer sequence contains a SmaI restriction
302     enzyme site followed by nucleotides corresponding to PTH receptor
303     coding sequence.
306 <400> SEQUENCE: 3
307 cagccgtccc ggccttgcc tgg                                     23
310 <210> SEQ ID NO: 4
311 <211> LENGTH: 27
312 <212> TYPE: DNA
313 <213> ORGANISM: Artificial Sequence
315 <220> FEATURE:
316 <221> NAME/KEY: Primer_Bind
317 <223> OTHER INFORMATION: This 3' primer sequence contains a SalI restriction
318     enzyme site and a sequence complementary to the human PTH
319     receptor.
321 <400> SEQUENCE: 4
322 cctcagtgtc gacttgtcat ccttcag                                     27
325 <210> SEQ ID NO: 5
326 <211> LENGTH: 27
327 <212> TYPE: DNA
328 <213> ORGANISM: Artificial Sequence
330 <220> FEATURE:
331 <221> NAME/KEY: Primer_Bind
332 <223> OTHER INFORMATION: This 5' primer contains a HindIII restriction enzyme site
333     and a nucleotide sequence corresponding to the 5' UTR of the cDNA
334     encoding human PTH receptor.
336 <400> SEQUENCE: 5
337 gttggcatat tggaagcttt ttgcggg                                     27
340 <210> SEQ ID NO: 6
341 <211> LENGTH: 28
342 <212> TYPE: DNA
343 <213> ORGANISM: Artificial Sequence
345 <220> FEATURE:
346 <221> NAME/KEY: Primer_Bind
347 <223> OTHER INFORMATION: This 3' primer sequence contains an XbaI restriction
348     enzyme site, a translation stop codon, and nucleotides
349     complementary to the human PTH receptor coding sequence.

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VERIFICATION SUMMARY

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L:9 M:270 C: Current Application Number differs, Replaced Current Application Number

L:10 M:271 C: Current Filing Date differs, Replaced Current Filing Date